Box Sea of 1646

PATENT
Attorney Docket No.: A-68294/DJB/RMS/DAV

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

LUO et al.

Serial No. 09/404,010

Filed: September 23, 1999

For: NOVEL TRAF4 ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE

Examiner: Andres, Janet

Group Art Unit: 1646

OIPE JC54 OCT 10 2000 PATENT & TRADEMARK OFFICE

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CERTIFICATE OF MAILING
I hereby certify that this correspondence, including listed enclosures, is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, DC 20231 on:

Dated: 10-4-00

Signed: Christine P. Peters
Christine P. Peters

TRANSMITTAL OF RESPONSE TO COMMUNICATION AND NOTICE TO COMPLY

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Assistant Commissioner
for Patents
Washington, DC 20231

Sir:

In response to the Office Communication and accompanying Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures dated September 5, 2000, enclosed are the following documents:

1. Copy of Communication and Notice to Comply;

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2. Replacement Paper copy of SEQUENCE LISTING;

3. Communication Re: Sequence Listing

4. Replacement Computer readable copy of Sequence Listing.

While no fee is currently believed to be due, the Commissioner is authorized to charge any additional fees, including any extension fees, which may be required, or credit any overpayment to Deposit Account No. 06-1300 (Our Order No. A-68294/DJB/RMS/DAV).

Respectfully submitted,

FLEHR HOHBACH TEST
ALBRITTON & HERBERT LLP

Dated: 10-4-00

Dolly A. Vance
Reg. 39,054

Four Embarcadero Center
Suite 3400
San Francisco, CA 94111-4187
Telephone: (415) 781-1989

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UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/404,010	09/23/99	LUO Y	A-68294/DJB/

HM22/0905
FLEHR HOHBACH TEST ALBRITTON & TEST LLP
FOUR EMBARCADERO CENTER STE 3400
SAN FRANCISCO CA 94111-4187

EXAMINER	
ANDRES, J	
ART UNIT	**PAPER NUMBER**
1646	8

DATE MAILED: 09/05/00

OIPE OCT 10 2000 JC54 PATENT & TRADEMARK OFFICE

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

File A-68294 Atty RMS/DAV
Due Date 10/5/00 3/5/01 of
Type Sequence Listing Refs

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PTO-90C (Rev. 2/95)

2 - Mail Copy

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UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/404010	9/23/99	Luo	A68294/DJB/

EXAMINER	
Janet Andres	
ART UNIT	PAPER NUMBER
1646	8

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CAR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CAR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

2. Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CAR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CAR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CAR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

3. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Janet Andres, Ph.D. whose telephone number is (703)305-0557. The examiner can normally be reached on Monday-Thursday from 8:00-5:30 pm (Eastern Time) and 8:00-4:30 PM every other Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, Ph.D., can be reached at (703)308-6564. The FAX phone number for group 1600 is (703)308-4242.

An inquiry of a general nature or relating to the status of the application should be directed to the group receptionist whose telephone number is (703)308-0196.

Yvonne Eyler

YVONNE EYLER, PH.D
PRIMARY EXAMINER

OIPE JC54 OCT 10 2000 TRADEMARK

Application No.: 09/404010

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- [ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other: Sequences in application that do not have a sequence id number

Applicant Must Provide:

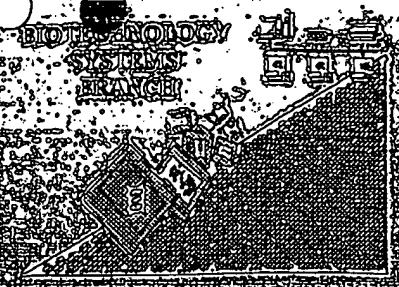
- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/404,010

Source: 1646

Date Processed by STIC: 7-26-00

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY; or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE - SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable Form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

BEST AVAILABLE COPY

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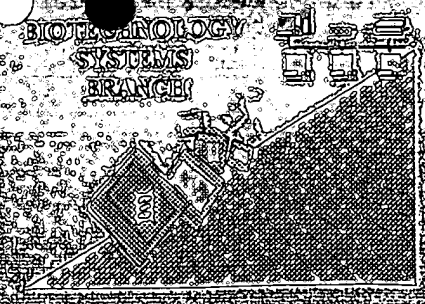

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/404,010

Source: 1646

Date Processed by STIC: 7-26-00

RECEIVED
AUG 16 2000
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY

or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

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Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/404,010

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

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1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

J. Andres

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RAW SEQUENCE LISTING DATE: 07/26/2000
PATENT APPLICATION: US/09/404,010 TIME: 14:25:18

Input Set : A:\A682941.app
Output Set: N:\CRF3\07262000\I404010.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Luo, Ying
4 Xu, Xiang
6 <120> TITLE OF INVENTION: Novel Traf4 Associated Cell Cycle Proteins,
7 Compositions and Methods of Use
9 <130> FILE REFERENCE: A68294/DJB/RMS/DAV
11 <140> CURRENT APPLICATION NUMBER: 09/404,010
12 <141> CURRENT FILING DATE: 1999-09-23
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

71 <210> SEQ ID NO: 2
72 <211> LENGTH: 832
73 <212> TYPE: RNA
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 2

Sequence contains "t's". Not allowed in RNA sequence.

E--> 77 nsgnnaEEaP gakaPEPaaa vgtnwFFard PvrdFPFELI PEPPEggLPg PwaLhrgrkk 60
E--> 78 atgsPvsIFv ydvkPgaEEQ tQvakaaFkr FktLrhPnIL ayIdgLEtEk cLhvvtEavt 120
E--> 79 PLgIyLkarv EaggLkELEI swgLhQIvka LsFLvndcsL Ihnnvcmaav FvdragEwkL 180
E--> 80 ggLdymysaQ gngggPPrkg IPELEQydPP ELadssgrvv rEkwsadmwr LgcLIwEvFn 240
E--> 81 gPLPraaaLr nPgkIPktLa PhycELvgan PkvrPnParF LQncraPggF msnrFvEtnL 300
E--> 82 FLEEIQIkEP aEkQkFFQEL sksLdaFPEd FcrhkLLPQL LtaFEFgnag avvLtPLFkv 360
E--> 83 gkFLsaEEyQ QkIIPvvvkm Fsstdramrl rLLQQmEQFI QyLdEPtvnt QIFPhvvhgF 420
E--> 84 LdtnPaIrEQ tvksmLLLaP kLnEanLnvE LmkhFarLQa kdEQgPIrqn ttvcLgkIgs 480
E--> 85 yLsastrhrv LtsaFsratr dPFaPsrvag vLgFaathnL ysmndcaQkI LPvLcgLtvd 540
E--> 86 PEksvrdQaF kaFrsFLskL EsvsEdPtQL EEvEkdvhaa ssPgmggaaa swagwavtgv 600
E--> 87 ssLtskLIrs hPttaPtEtn IPQrPtPEgv PaPaPtPvPa tPttsghwEt QEEdkdtaEd 660
E--> 88 sstadrwddE dwgsLEQEaE svLaQQddws tggQvsrasQ vsnsdhkssk sPEsdwsswE 720
E--> 89 aEgswEQgwQ EPssQEPPsd gtrLasEynw ggPEssdkgd PFatLsarPs tQPrPdswgE 780
E--> 90 dnwEgLEtds rQvkaELark krEErrrEmE akraErkvak gPmkLgarkL dZ 832

Sequence contains "n's". As per sequence rules, "n's" must be addressed in <220> to <223> feature.

Letters in upper case are not valid base identifiers.

* See #10 on Error Summary Sheet

VERIFICATION SUMMARY DATE: 07/26/2000
PATENT APPLICATION: US/09/404,010 TIME: 14:25:19

Input Set : A:\A682941.app
Output Set: N:\CRF3\07262000\I404010.raw

L:77 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:77 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:77 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:77 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:77 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:25
L:77 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:1
L:77 M:112 C: (48) String data converted to lower case,
L:78 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:78 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:78 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:78 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:78 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:26
L:78 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7
M:112 Repeated in SeqNo=2
L:79 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:79 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:21
L:79 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7
L:80 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:80 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:80 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7
L:81 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:81 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:24
L:81 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:9
L:82 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:82 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:36
L:82 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:11
L:83 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:83 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:31
L:83 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:14
L:84 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:84 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/404,010

DATE: 07/26/2000
TIME: 14:25:19

Input Set : A:\A682941.app
Output Set: N:\CRF3\07262000\I404010.raw

L:84 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:84 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:84 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:27
L:84 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:18
L:85 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:85 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:85 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:23
L:86 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19
L:86 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:25
L:87 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:87 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:35
L:87 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:37
L:88 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:88 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:88 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:88 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:88 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:88 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:39
L:89 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:89 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:25
L:89 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:42
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:90 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:90 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:43

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